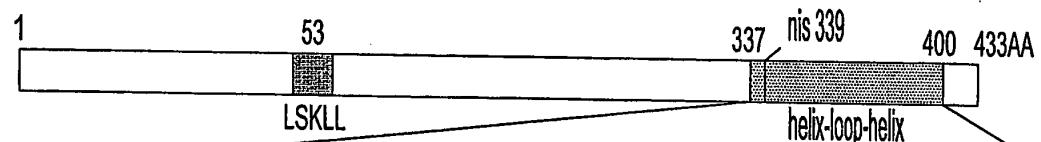
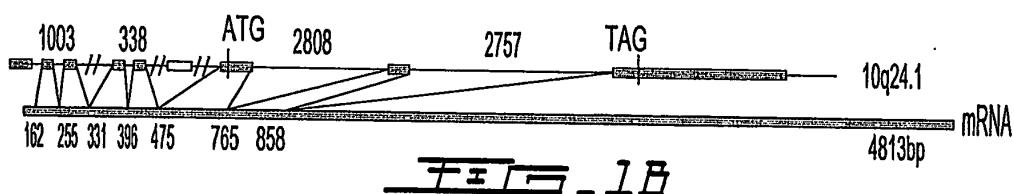
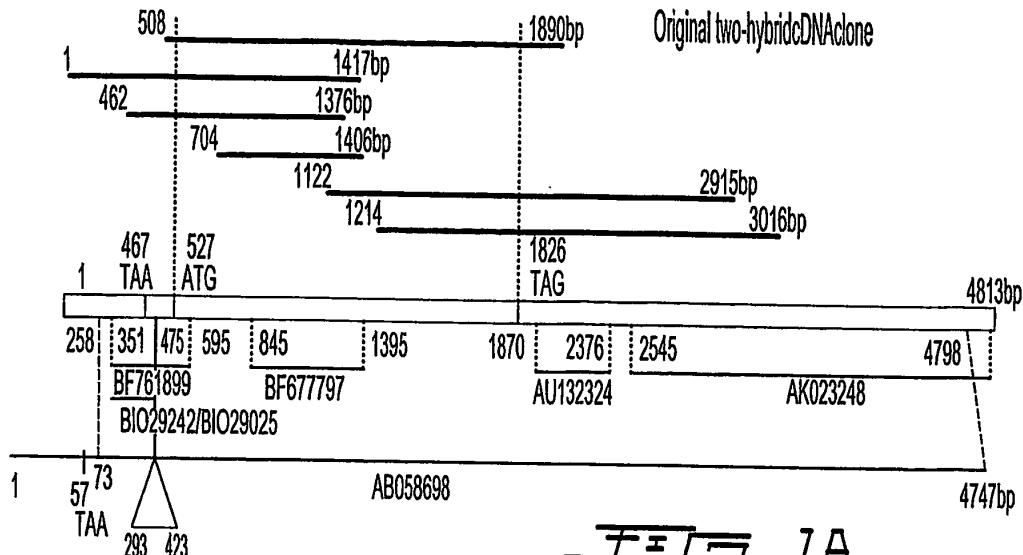


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CCACGACAACCCACTGCAAGCAGATCCAGCAGCTGCTTCTGTAAATGCAGGACTCCCCAGGAGCACCCAGGCATGGGCAGCAACCCCTGCA	91
TGCCATTCTTTGGCTCCCGAGAACAGGAGATAAACACCACCATCATCTGAGAGCCGGAAAGGGAGGGCTGTGTAGGCGGCAC	183
GAATGCTCCGTTGAGAGACGCCCTTCGGCAAGAAGTGGATTCTGGCCACAAGCTCATTCACTGTGTAGGTCCCGTTCCCTGTGCG	275
GGCGGCCGGGGACCATAAGGCCTTAACCTCATATTTAACCCCCCTCCAAAAGGTTGAAAGTATTCTGAAGGGCTGTTGGACCTGC	367
ATTATTAAGATCTCAGTTATTAAAGACTGTGAACCTGAAAGCATTCTGATTGGACTTTGATGAAAAGTGTATTCTGTTGA	459
M Q R M I Q	6
GAAGAGATAAAAGTAAAGACAGTCCCTGGGCTCCGACCCCAATATTCCCTAGTGGCCGTGAGATC ATG CAG CGA ATG ATC CAA	544
[Q F A A E] Y T S K N S S T Q D P S Q P N S T K	29
CAA TTT GCT GCT GAA TAT ACC TCA AAA AAT AGC TCT ACT CAG GAC CCC AGC CAG CCC AAT AGC ACA AAG	613
N Q S L P K A S P V T T S P T A A T T Q N P V	52
AAC CAA ACC CTG CCG AAA GCA TCT CCA GTC ACC ACC TCT CCC ACG GCT GCA ACT ACT CAG AAC CCT GTG	682
L S K L L M A D Q D S P L D L T V R K S Q S E	75
CTC AGC AAA CTT CTC ATG GCT GAC CAA GAC TCA CCT CTG GAC CTT ACT GTC AGA AAG TCT CAG TCA GAA	751
P S E Q D G V L D L S T K K S P C A G S T S L	98
CCT AGC GAA CAA GAC GGT GTA CTT GAT CTG TCC ACT AAG AAA AGT CCA TGT GCT GGC AGC ACT TCC CTG	820
S H S P G C S S T Q G N G R P G R P S Q Y R P	121
AGC CAC TCT CCA GGC TGC TCC AGT ACT CAA GGG AAC GGG CGA CCT GGG AGA CCC AGC CAG TAC CGC CCA	889
D G L R S G D G V P P R S L Q D G T R E G F G	144
GAC GGA CTT CGG AGT GGT GAT GGG GTA CCT CCA AGA AGC TTA CAG GAT GGA ACC AGG GAA GGT TTT GGA	958
H S T S L K V P L A R S L Q I S E E L L S R N	167
CAC TCC ACA TCA CTC AAA GTT CCA CTG GCT CGA TCC CTG CAG ATT AGT GAA GAA CTA CTG AGC AGA AAC	1027

FIG - 10

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Q	L	S	T	A	A	S	L	G	P	S	G	L	Q	N	H	G	Q	H	L	I	L	S	190
CAA	TTG	TCC	ACA	GCT	GCC	AGC	CTT	GGG	CCA	TCT	GGA	TTA	CAG	AAT	CAT	GGA	CAA	CAC	TTA	ATA	TTA	TCC	1096
R	E	A	S	W	A	K	P	H	Y	E	F	N	L	S	R	M	K	F	R	G	N	G	213
AGG	GAA	GCC	TCT	TGG	GCA	AAA	CCA	CAT	TAC	GAG	TTC	AAC	CTC	AGC	CCT	ATG	AAG	TTC	AGG	GGA	AAT	GGT	1165
A	L	S	N	I	S	D	L	P	F	L	A	E	N	S	A	F	P	K	M	A	L	Q	236
GCA	CTC	AGC	AAC	ATC	AGT	GAC	CTT	CCT	TTT	CTT	GCA	GAA	AAC	TCT	GCC	TTT	CCA	AAA	ATG	GCA	CTT	CAA	1234
A	K	Q	D	G	K	K	D	V	S	H	S	S	P	V	D	L	K	I	P	Q	V	R	259
GCA	AAA	CAA	GAT	GGA	AAA	AAG	GAT	GTG	AGC	CAT	TCA	TCT	CCT	GTA	GAT	TTA	AAG	ATA	CCA	CAA	GTT	CGA	1303
G	M	D	L	S	W	E	S	R	T	G	D	Q	Y	S	Y	S	S	L	V	M	G	S	282
GGA	ATG	GAT	CTT	TCT	TGG	GAG	TCT	CGC	ACT	GGT	GAT	CAG	TAC	AGC	TAT	AGC	TCT	TTG	GTA	ATG	GGT	TCA	1372
Q	T	E	S	A	L	S	K	K	L	R	A	I	L	P	K	Q	S	R	K	S	M	L	305
CAA	ACG	GAG	AGC	GCG	CTT	AGT	AAA	AAA	TTA	AGG	GCT	ATT	CTT	CCA	AAA	CAA	AGT	AGA	AAA	AGC	ATG	TTA	1441
D	A	G	P	D	S	W	G	S	D	A	E	Q	S	T	S	G	Q	P	Y	P	T	S	328
GAT	GCT	GGA	CCC	GAT	TCT	TGG	GGC	TCA	GAT	GCT	GAG	CAG	TCT	ACC	TCT	GGA	CAG	CCA	TAT	CCC	ACA	TCG	1510
D	Q	E	G	D	P	G	S	[REDACTED]	351														
GAT	CAA	GAA	GGA	GAC	CCT	GGC	TCC	AAG	CAG	CCT	CGG	AAG	AAA	AGA	GGG	CGT	TAC	AGA	CAG	TAC	AAC	AGT	1579
[REDACTED]	374																						
GAG	ATA	CTG	GAG	GAA	GCA	ATC	TCA	GTG	GTT	ATG	AGT	GGA	AAA	ATG	AGT	GTT	TCC	AAA	GCT	CAG	AGT	ATT	1648
[REDACTED]	397																						
TAT	GGG	ATT	CCC	CAC	AGT	ACA	CTG	GAG	TAC	AAA	GTA	AAG	GAG	AGG	CTG	GGC	ACT	TTG	AAA	AAC	CCT	CCA	1717
K	K	K	M	K	L	M	R	S	E	G	P	D	V	S	V	K	I	E	L	D	P	Q	420
AAG	AAA	AAG	ATG	AAA	TTA	ATG	AGG	TCG	GAG	GGG	CCA	GAT	GTT	TCT	GTA	AAG	ATT	GAA	TTA	GAT	CCC	CAG	1786
G	E	A	A	Q	S	A	N	E	S	K	N	E	*										433
GGA	GAG	GCA	GCA	CAA	AGT	GCA	AAT	GAA	TCA	AAA	AAC	GAG	TAG										1828

~~7-10~~ - 10 (CONTINUE)

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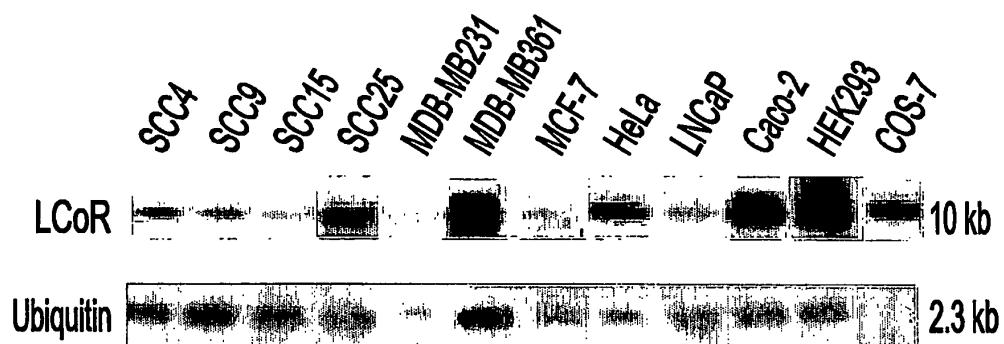
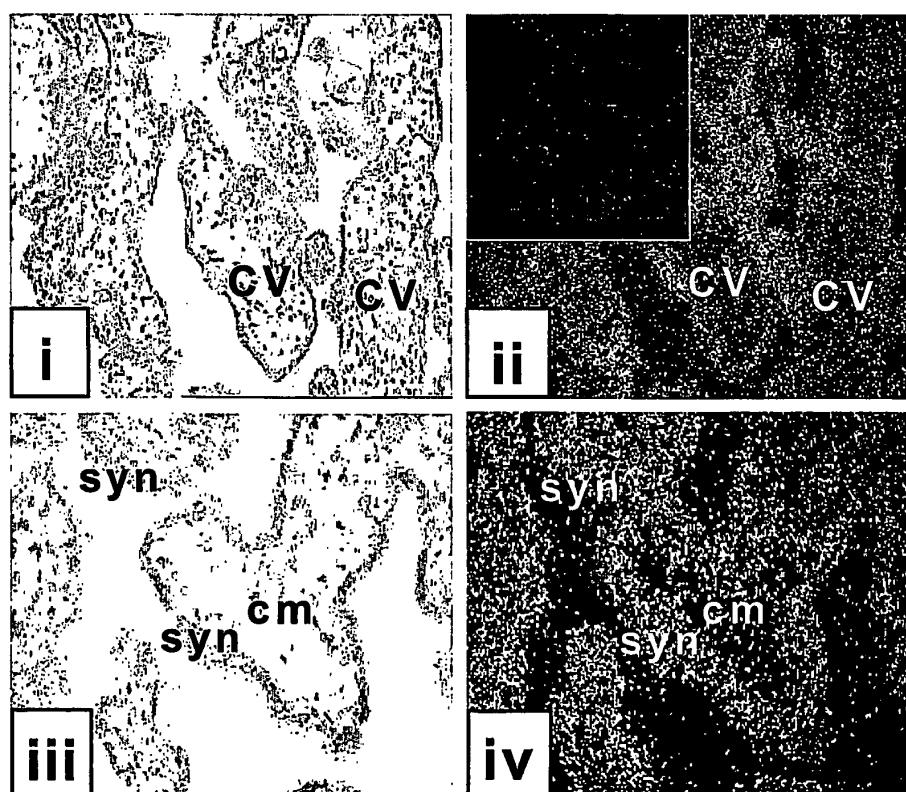
	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	accumbens nucleus	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast rRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	<i>E. coli</i> rRNA
D	pariental lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	<i>E. coli</i> DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricule, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	Poly r(A)
F	temporal lobe	hippo-campus		ventricule, right	iliocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human Cyt 1 DNA
G	p.g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma, SW480	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 ng

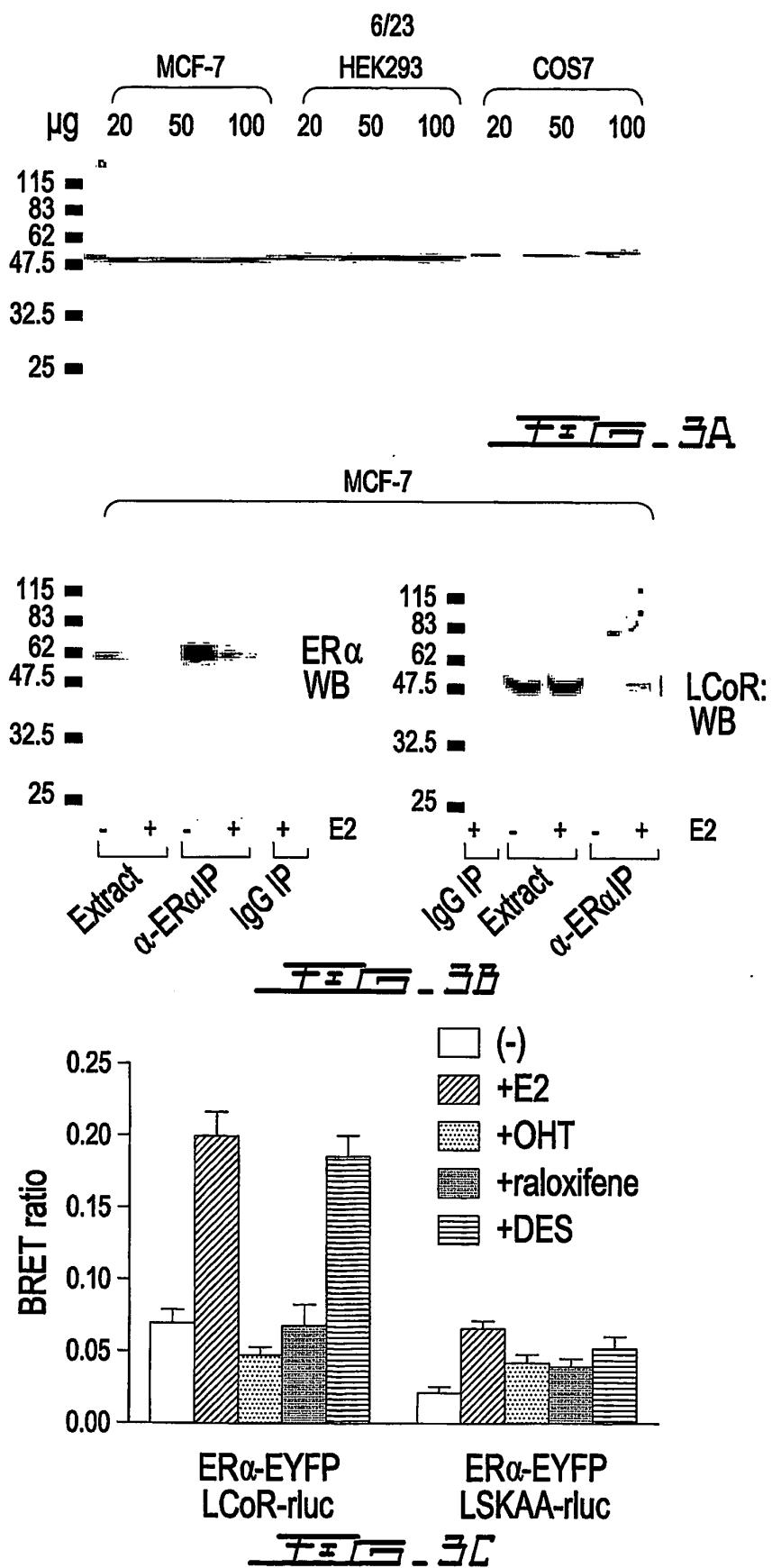
*paracentral gyrus

	1	2	3	4	5	6	7	8	9	10	11	12
A	*	*	*	*	*	*	*	*	*	*	*	*
B	*	*	*	*	*	*	*	*	*	*	*	*
C	*	*	*	*	*	*	*	*	*	*	*	*
D	*	*	*	*	*	*	*	*	*	*	*	*
E	*	*	*	*	*	*	*	*	*	*	*	*
F	*	*	*	*	*	*	*	*	*	*	*	*
G	*	*	*	*	*	*	*	*	*	*	*	*
H	*	*	*	*	*	*	*	*	*	*	*	*

T35 - 2A

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~~FEB - 2B~~~~FEB - 2C~~



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Input LCOR
GST alone
E2 +E2 +OHT +Ral +Cl

GST-ER α LBD

Input ER α
GST alone
E2 +E2 +E2 +E2 +E2 +E2

GST-LCOR GST-LSKAA GST-TF-2.1

50 -

67 -

75-4A75-4B

Input LCOR
GST alone
E2 +E2 +E2 +E2 +E2

GST-LCOR GST-ER α H12-

Input ER378
GST alone
E2 +E2 +E2 +E2 +E2 +E2

GST-LCOR GST-LSKAA GST-TF-2.1

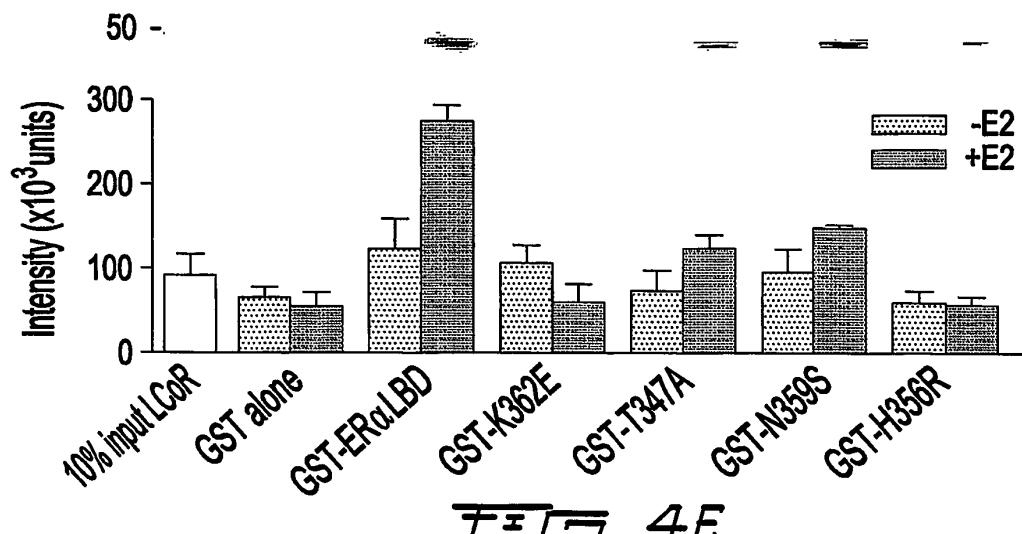
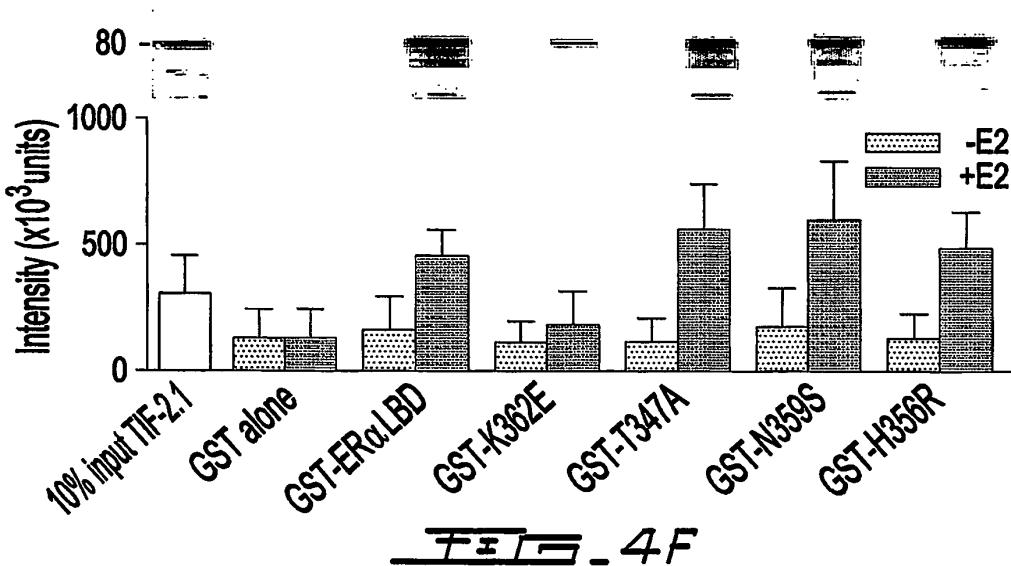
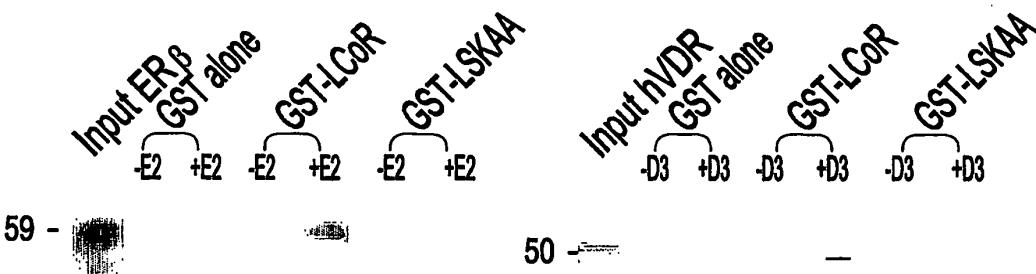
50 -

45 -

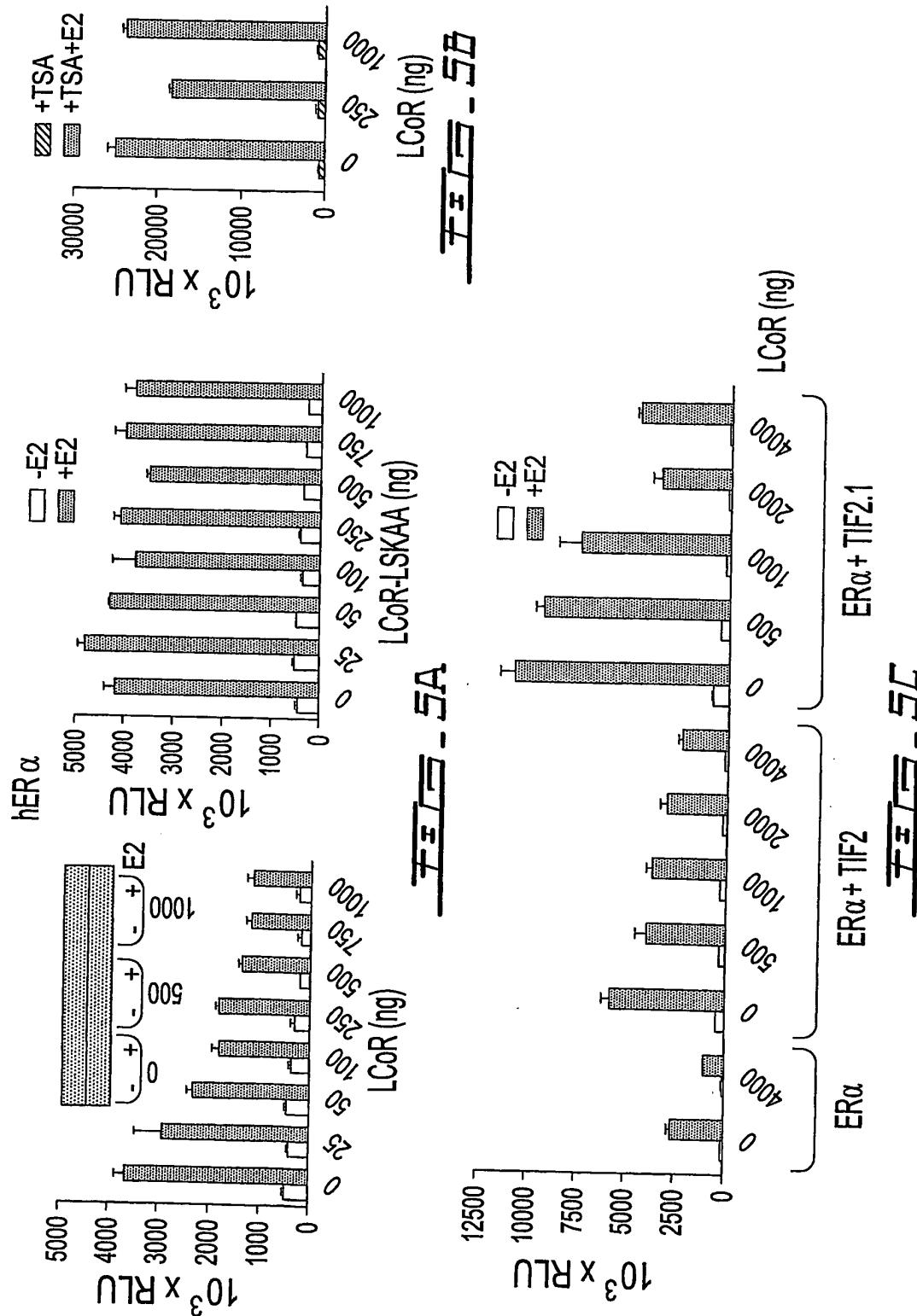
T

75-4C75-4D

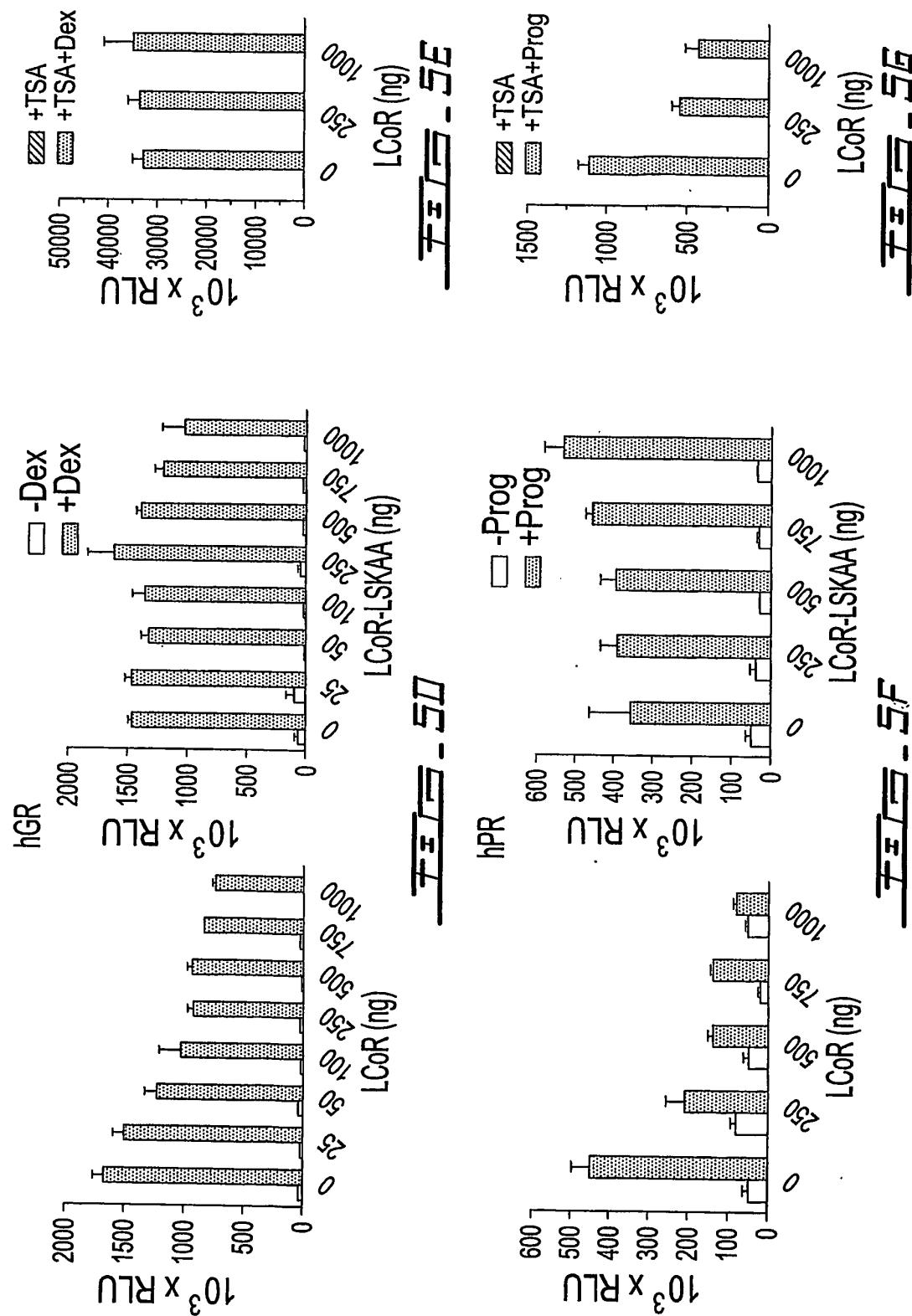
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TIF-4ETIF-4FTIF-4GTIF-4H

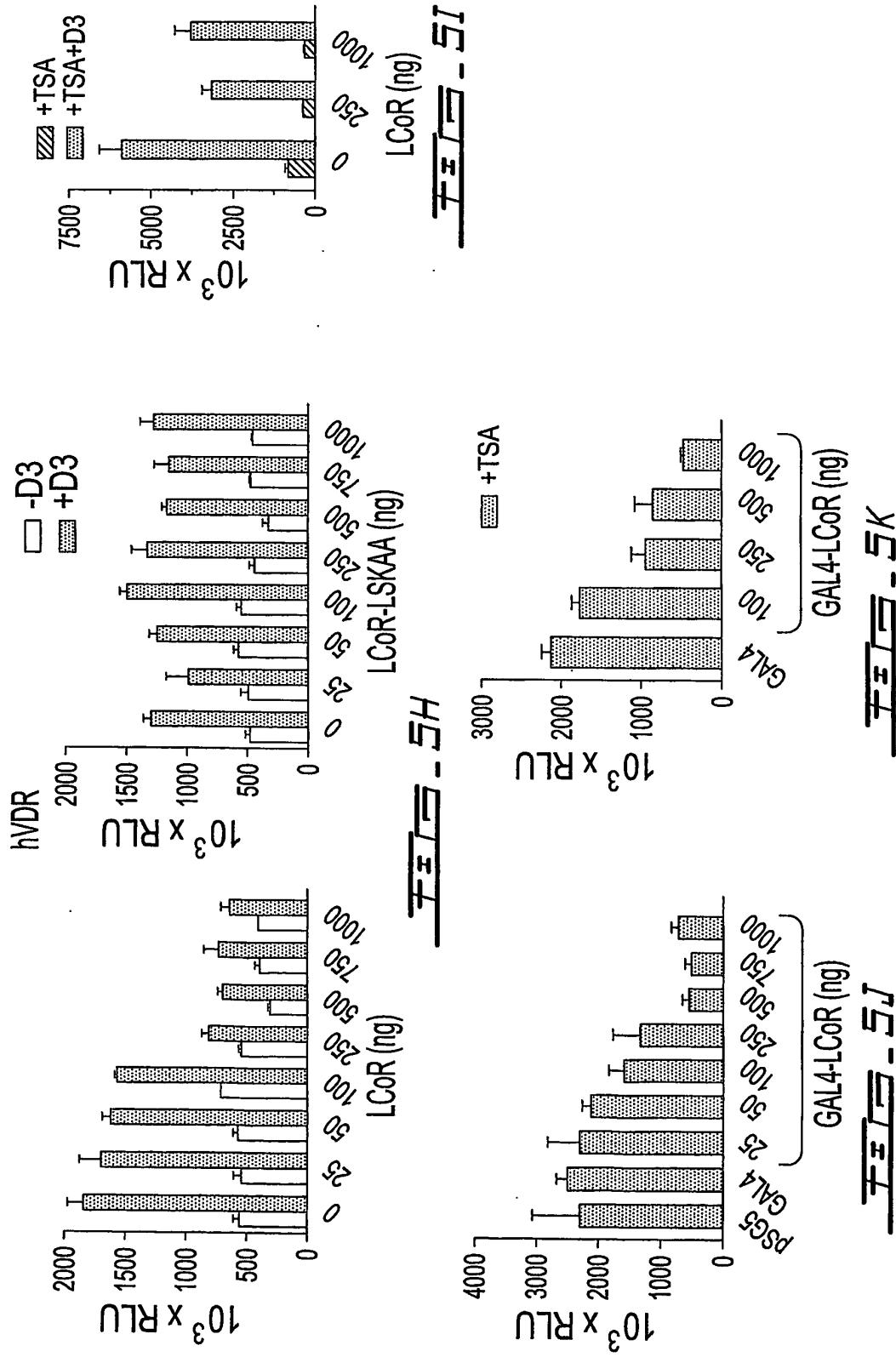
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Input HDAC3 Input HDAC7
GST alone GST alone
GST-LCKR GST-LCKA
GST-LSKA GST-LSKM
GST-LCKB GST-LCKM
GST alone GST alone
GST-LCKR GST-LCKA
GST-LSKA GST-LSKM
GST-LCKB GST-LCKM

49

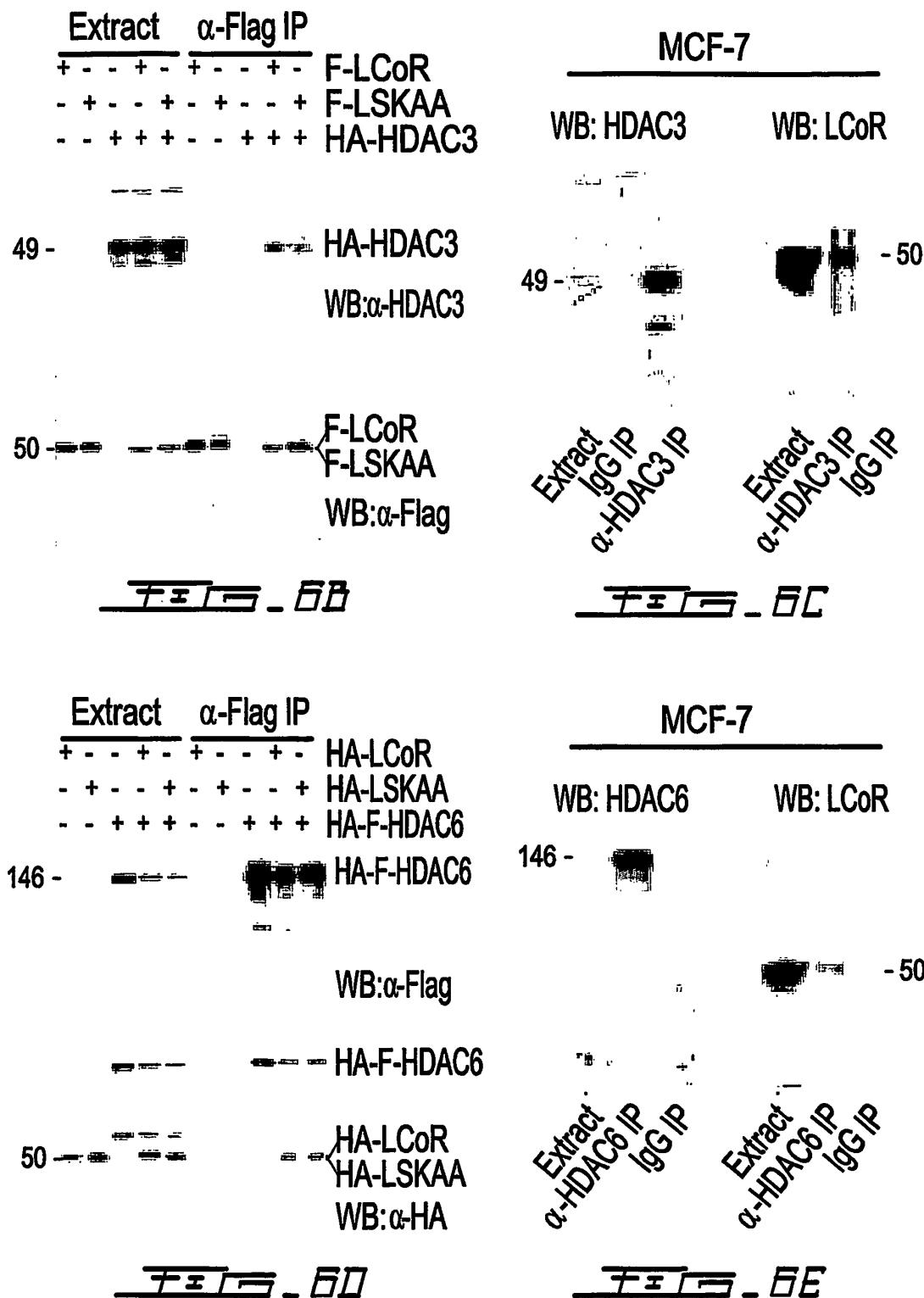
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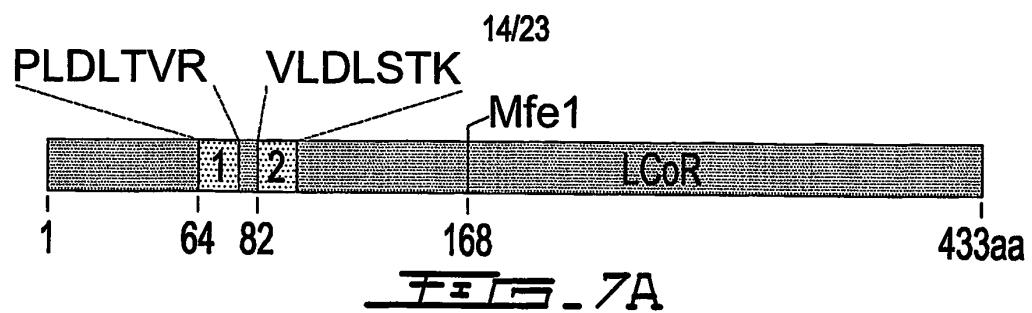
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- 125 -

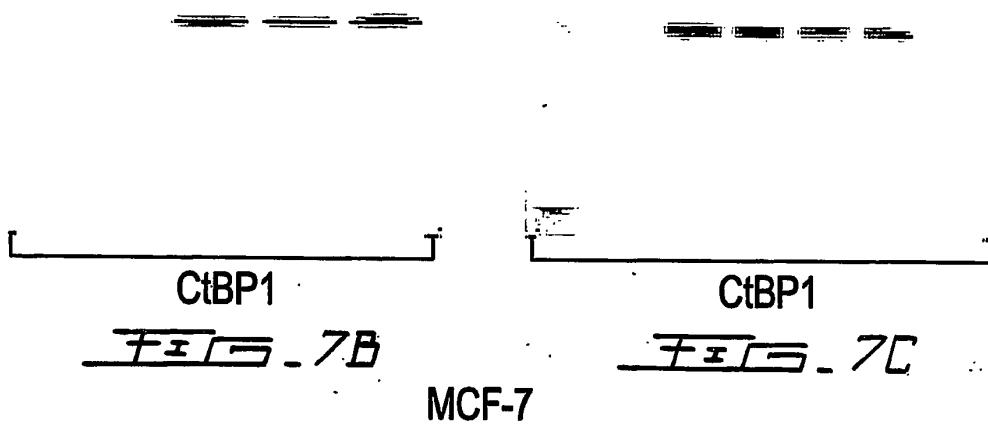
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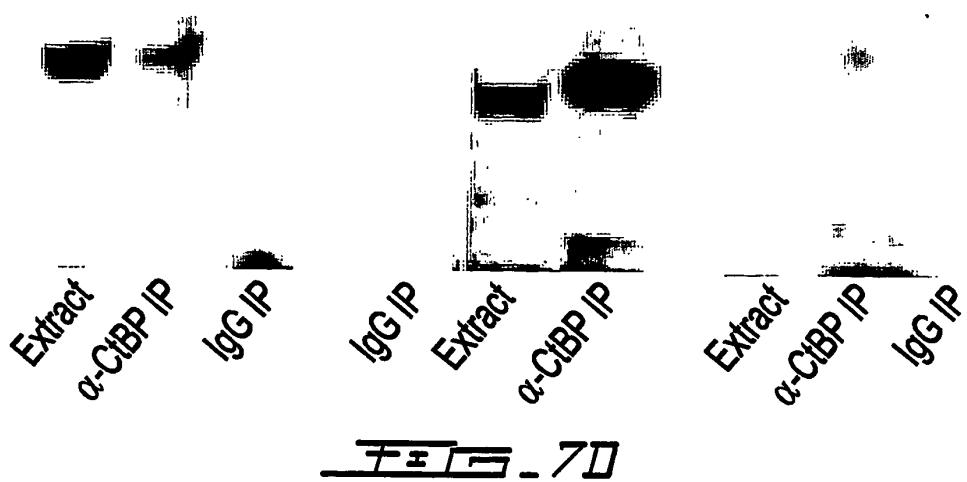




Input	pGEX	GST-LCoR	GST-LSKAA	GST-LCoR-Mfe1	Input	pGEX	GST-LCoR	GST-LSKAA	GST-m1	GST-m2	GST-m1+2
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MCF-7

WB: LCoR	WB: CtBP1	WB: CtBP2
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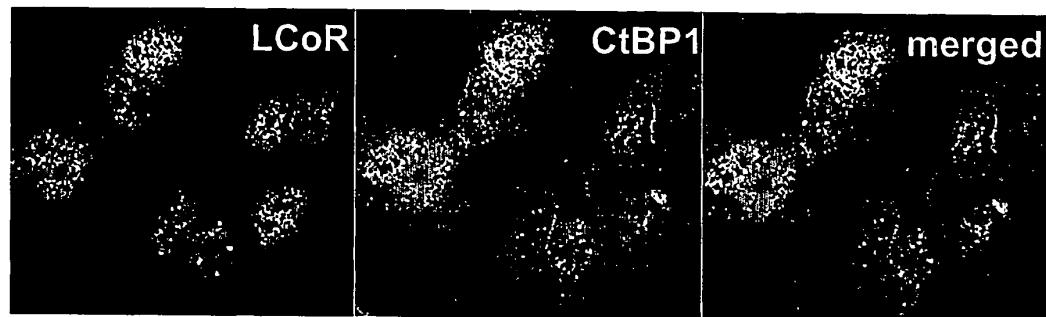


FIG-7E

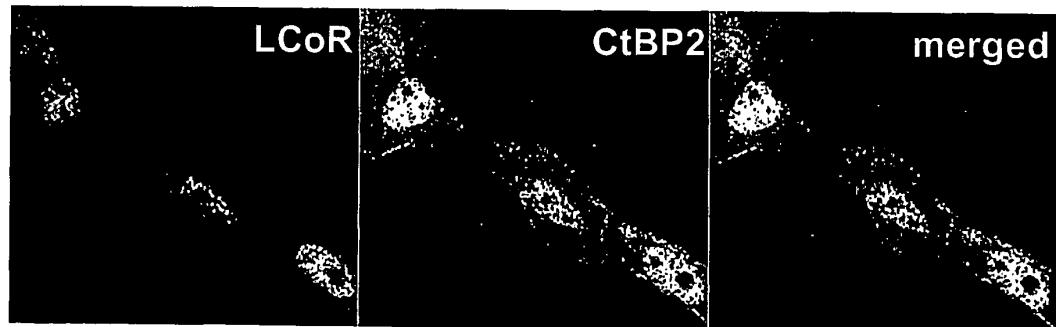
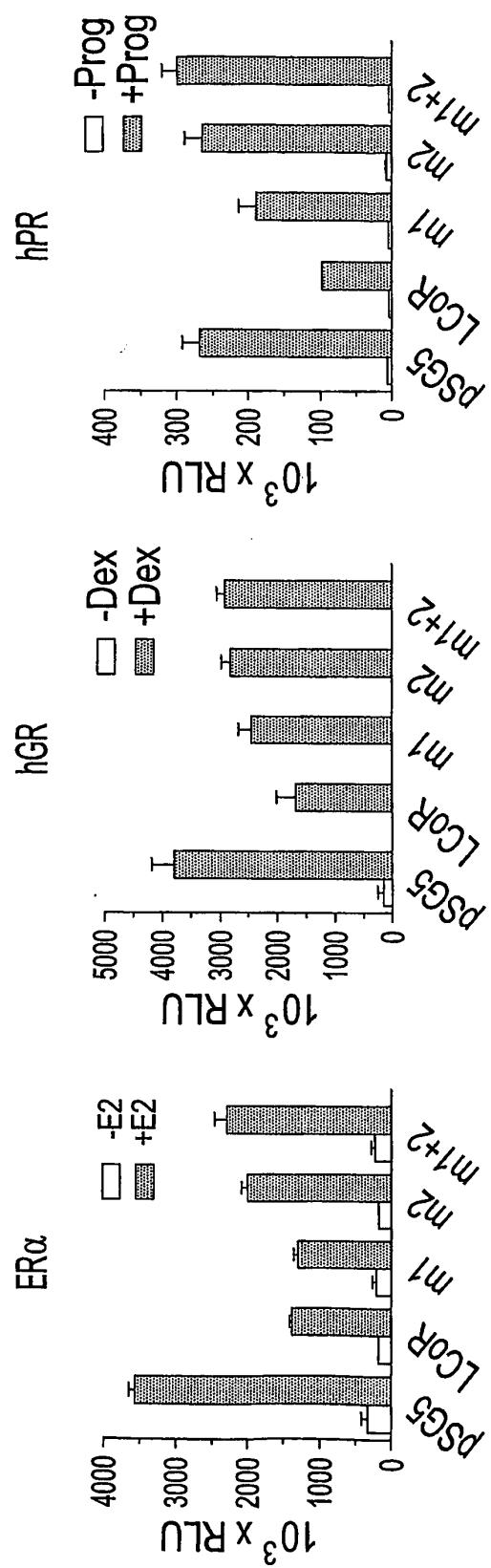
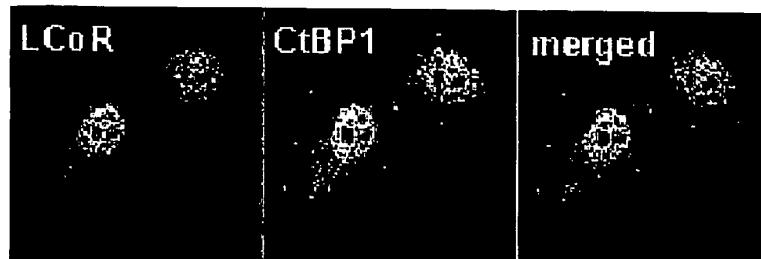
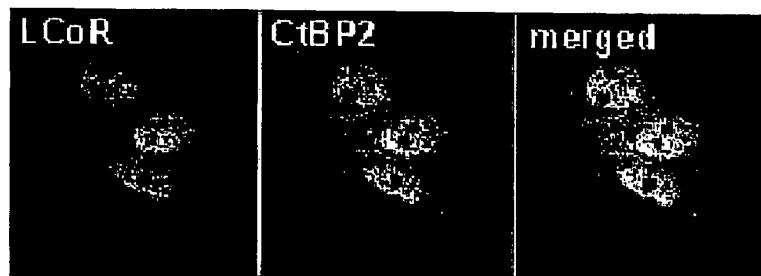
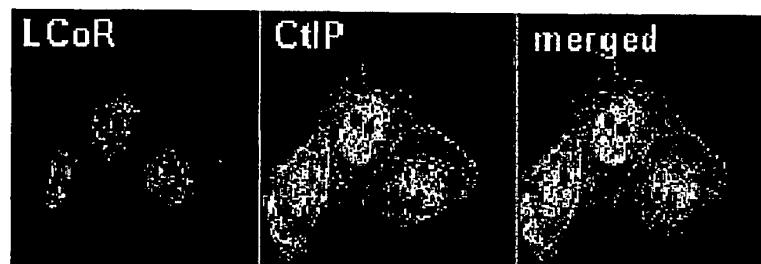
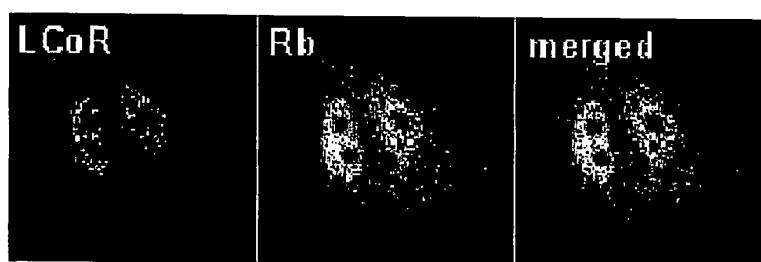
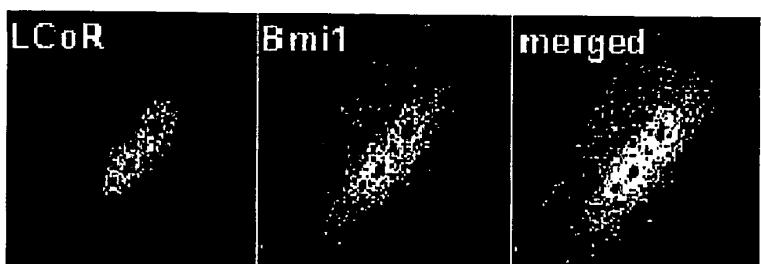


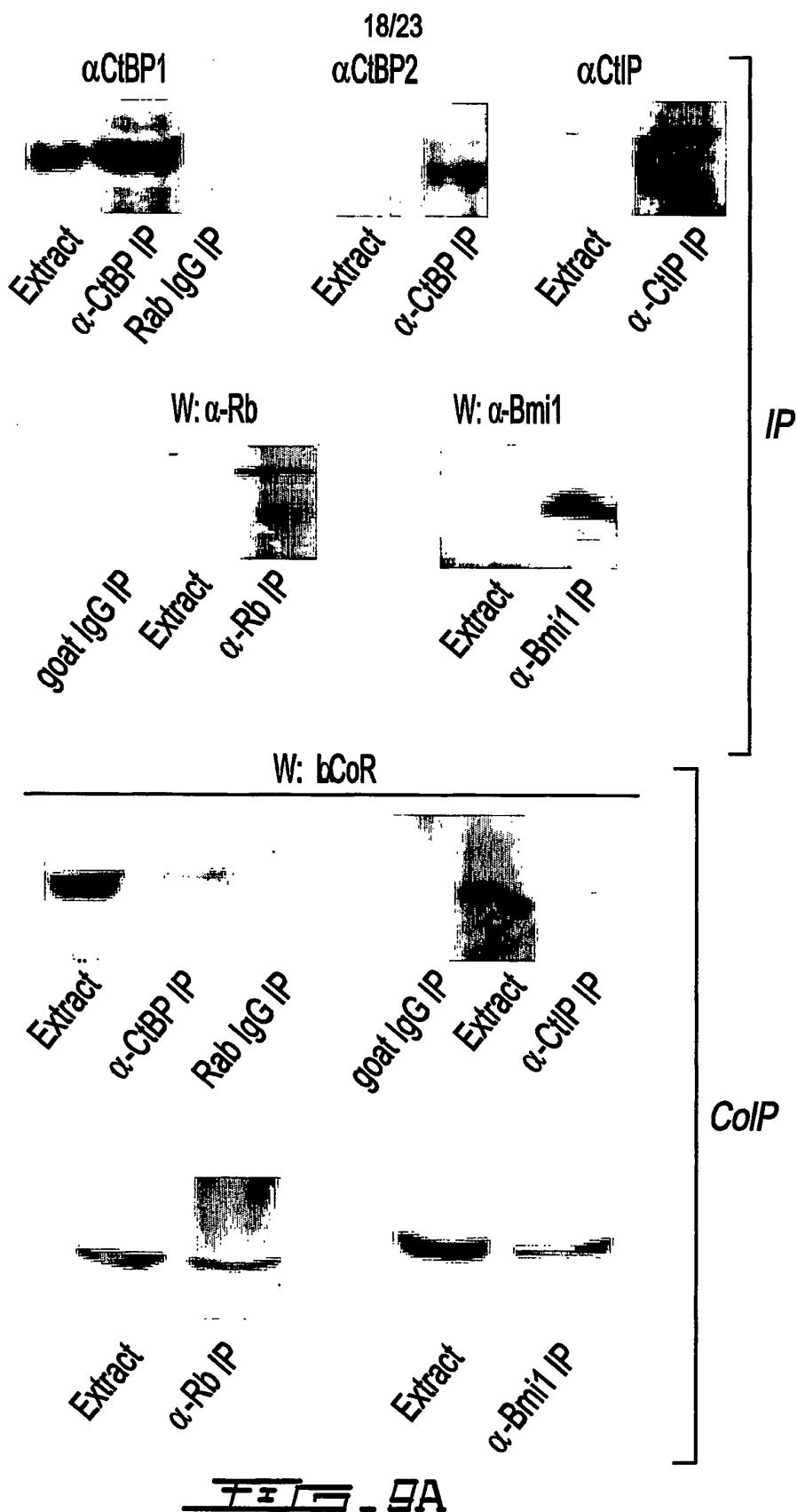
FIG-7F

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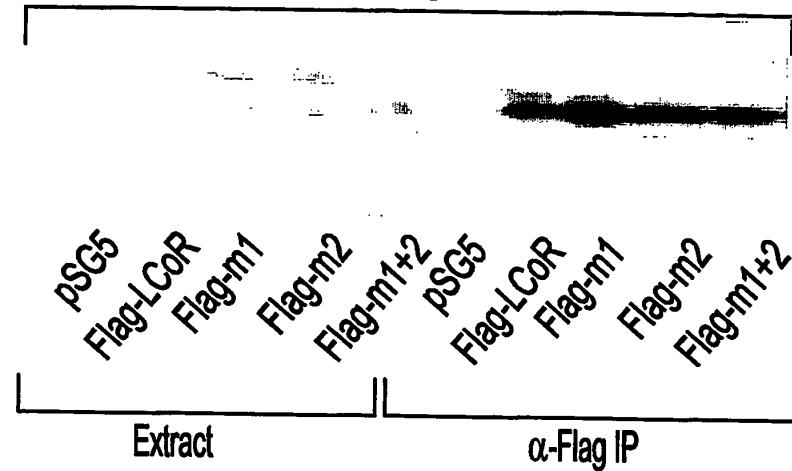
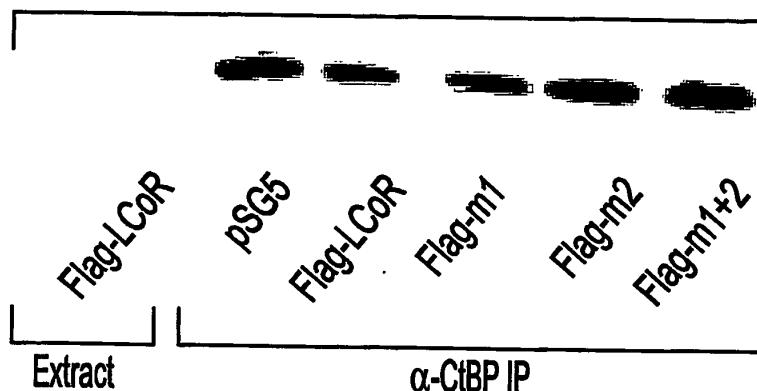
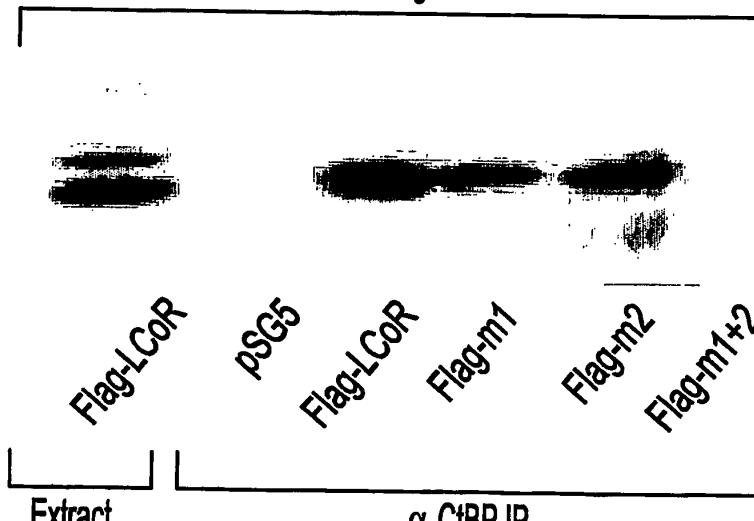
~~TEST - 7E~~

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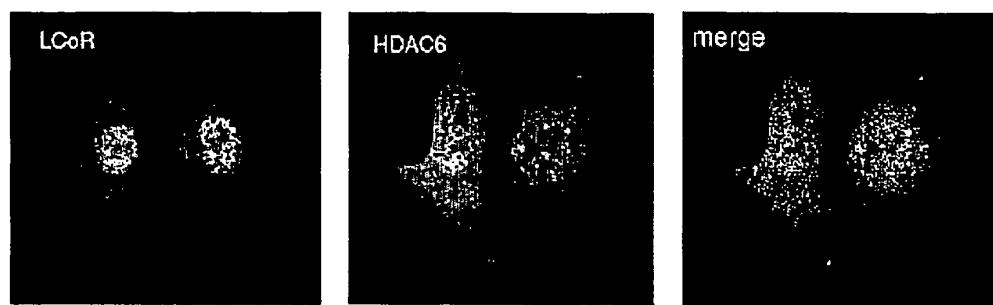
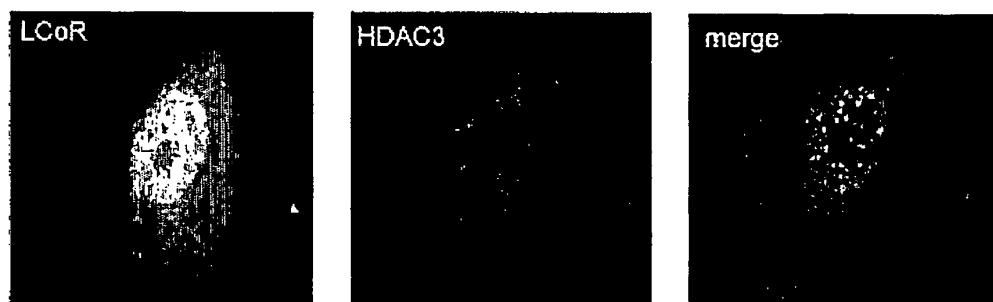
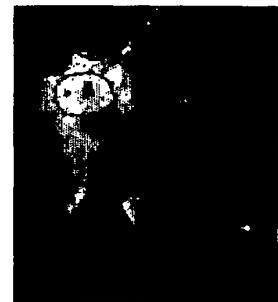
~~TIG - BA~~~~TIG - BB~~~~TIG - BC~~~~TIG - BD~~~~TIG - BE~~



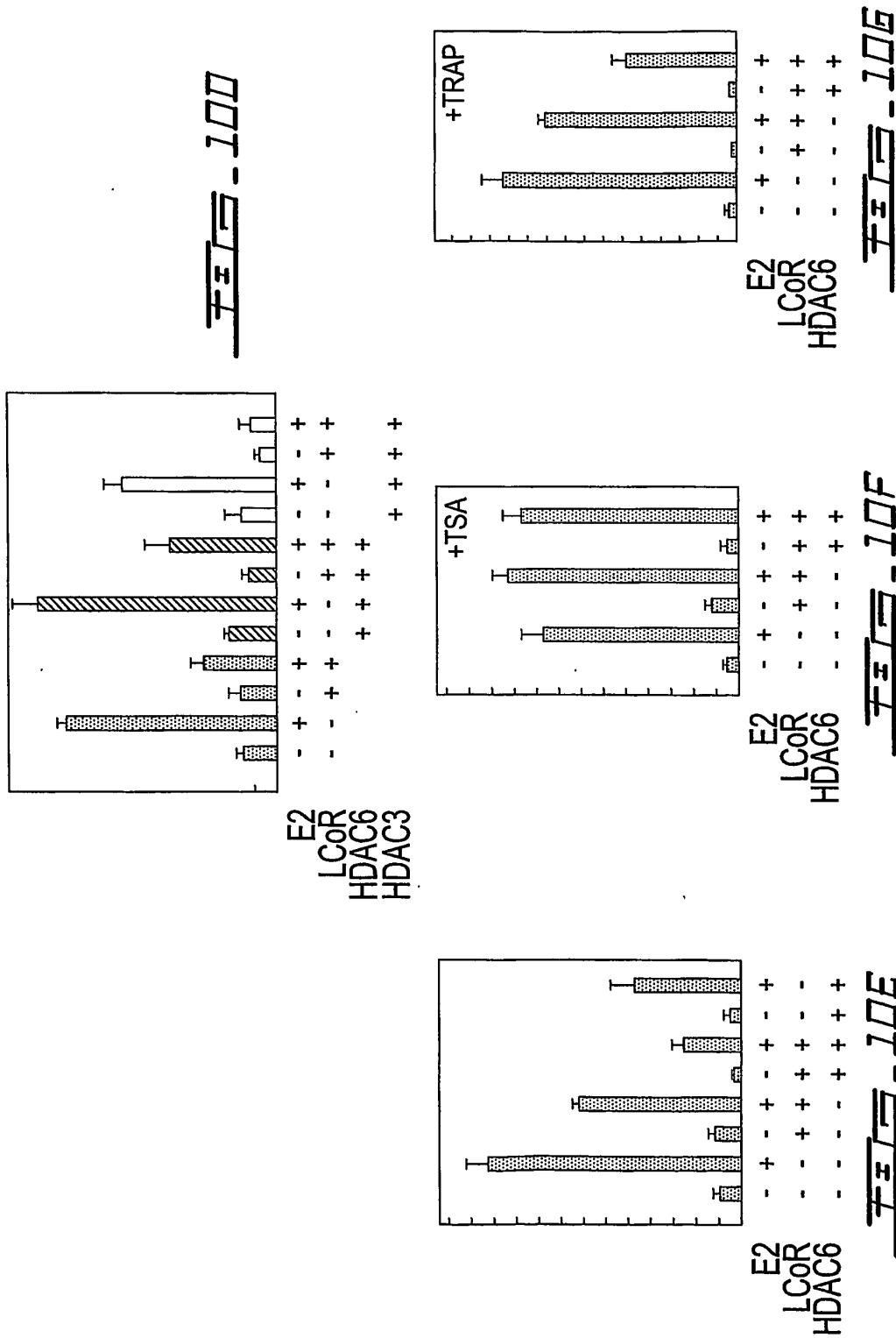
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 α -Flag α -CtBP1 α -Flag~~FEB - 98~~

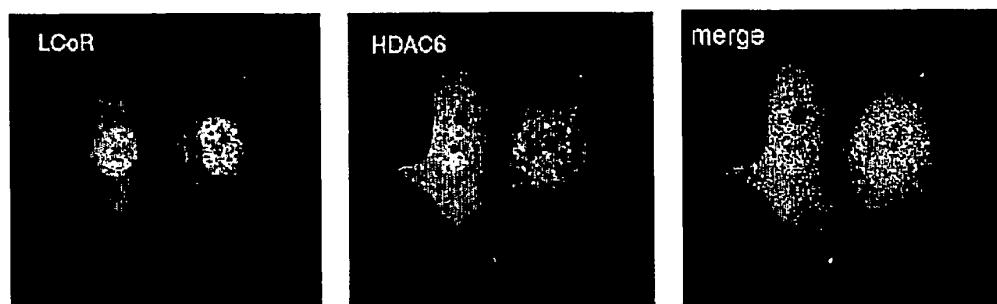
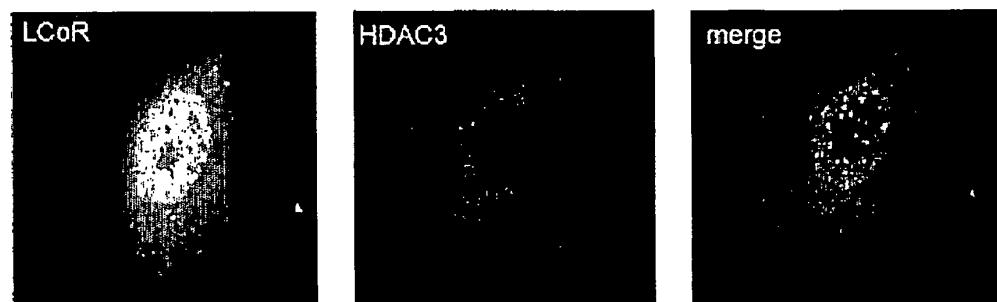
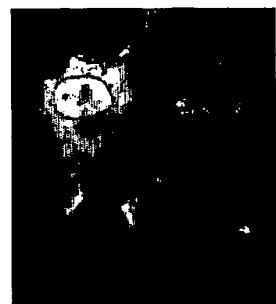
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FIG - 10AFIG - 10BFIG - 10C

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FIG - 11AFIG - 11BFIG - 11C

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